SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: LASKY, LAURENCE A.
STACHELL, SCOTT E.
ROSEN, STEVEN D.
SINGER, MARK S.
YEDNOCK, TED A.

(ii) TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:
   (A) ADDRESSEE: Genentech, Inc.
   (B) STREET: 1 DNA Way
   (C) CITY: South San Francisco
   (D) STATE: California
   (E) COUNTRY: USA
   (F) ZIP: 94080

(v) COMPUTER READABLE FORM:
   (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
   (B) COMPUTER: IBM PC compatible
   (C) OPERATING SYSTEM: PC-DOS/MS-DOS
   (D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:
   (A) APPLICATION NUMBER:
   (B) FILING DATE: 20-Jul-1998
   (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

    (A) APPLICATION NUMBER: 08/513278

    (B) FILING DATE: 10

(vii) PRIOR APPLICATION DATA:

    (A) APPLICATION NUMBER: 08/059027

    (B) FILING DATE: AUG-1995

(vii) PRIOR APPLICATION DATA:

    (A) APPLICATION NUMBER: 07/786149

    (B) FILING DATE: 6-MAY1993

(vii) PRIOR APPLICATION DATA:

    (A) APPLICATION NUMBER: 07/315015

    (B) FILING DATE: 31-OCT-1991

(viii) ATTORNEY/AGENT INFORMATION:

    (A) NAME: Dreger, Ginger R.

    (B) REGISTRATION NUMBER: 33,055

    (C) REFERENCE/DOCKET NUMBER: P0565D1C3

(ix) TELECOMMUNICATION INFORMATION:

    (A) TELEPHONE: 650/225-3216

    (B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

  (i) SEQUENCE CHARACTERISTICS:

    (A) LENGTH: 2259 base pairs

    (B) TYPE: Nucleic Acid

    (C) STRANDEDNESS: Single

    (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCCAGT GTGCTGGCTT CCTCACCTGC AGCACAGCAC ACTCCCTTTG 50

GCAAGGACCT GAGACCCTTG TGCTAAGTCA AGAGGCTCAA TGGGCTGCAG 100

AAGAACTAGA GAAGGACCAA GCAAAGCCAT GATATTTCCA TGGAAATGTC 150

AGAGCACCCA GAGGGACTTA TGGAACATCT TCAAGTTGTG GGGGTGGACA 200

ATGCTCTGTT GTGATTTCCT GGCACATCAT GGAACCTACT GCTGGACTTA 250

CCATTATTCT GAAAAACCCA TGAACTGGCA AAGGGCTAGA AGATTCTGCC 300

GAGACAATTA CACAGATTTA GTTGCCATAC AAAACAAGGC GGAAATTGAG 350

TATCTGGAGA AGACTCTGCC CTTCAGTCGT TCTTACTACT GGATAGGAAT 400

CCGGAAGATA GGAGGAATAT GGACGTGGGT GGGAACCAAC AAATCTCTCA 450

CTGAAGAAGC AGAGAACTGG GGAGATGGTG AGCCCAACAA CAAGAAGAAC 500

AAGGAGGACT GCGTGGAGAT CTATATCAAG AGAAACAAAG ATGCAGGCAA 550

ATGGAACGAT GACGCCTGCC ACAAACTAAA GGCAGCCCTC TGTTACACAG 600

CTTCTTGCCA GCCCTGGTCA TGCAGTGGCC ATGGAGAATG TGTAGAAATC 650

ATCAATAATC ACACCTGCAA CTGTGATGTG GGGTACTATG GGCCCCAGTG 700

TCAGCTTGTG ATTCAGTGTG AGCCTTTGGA GGCCCCAGAG CTGGGTACCA 750

62

TGGACTGTAC TCACCCCTTT GGAAACTTCA GCTTCAGCTC ACAGTGTGCC 800

TTCAGCTGCT CTGAAGGAAC AAACTTAACT GGGATTGAAG AAACCACCTG 850

TGGACCATTT GGAAACTGGT CATCTCCAGA ACCAACCTGT CAAGTGATTC 900

AGTGTGAGCC TCTATCAGCA CCAGATTTGG GGATCATGAA CTGTAGCCAT 950

CCCCTGGCCA GCTTCAGCTT TACCTCTGCA TGTACCTTCA TCTGCTCAGA 1000

AGGAACTGAG TTAATTGGGA AGAAGAAAC CATTTGTGAA TCATCTGGAA 1050

TCTGGTCAAA TCCTAGTCCA ATATGTCAAA AATTGGACAA AGTTTCTCA 1100

ATGATTAAGG AGGGTGATTA TAACCCCCTC TTCATTCCAG TGGCAGTCAT 1150

GGTTACTGCA TTCTCTGGGT TGGCATTTAT CATTTGGCTG GCAAGGAGAT 1200

TAAAAAAAGG CAAGAAATCC AAGAGAAGTA TGAATGACCC ATATTAAATC 1250

GCCCTTGGTG AAAGAAAATT CTTGGAATAC TAAAAATCAT GAGATCCTTT 1300

AAATCCTTCC ATGAAACGTT TTGTGTGGTG GCACCTCCTA CGTCAAACAT 1350

GAAGTGTGTT CCTTCAGTGC ATCTGGGAAG ATTTCTACCC GACCAACAGT 1400

TCCTTCAGCT TCCATTTCGC CCCTCATTTA TCCCTCAACC CCCAGCCCAC 1450

AGGTGTTTAT ACAGCTCAGC TTTTTGTCTT TTCTGAGGAG AAACAAATAA 1500

GACCATAAGG GAAAGGATTC ATGTGGAATA TAAAGATGGC TGACTTTGCT 1550

CTTTCTTGAC TCTTGTTTTC AGTTTCAATT CAGTGCTGTA CTTGATGACA 1600

GACACTTCTA AATGAAGTGC AAATTTGATA CATATGTGAA TATGGACTCA 1650

GTTTTCTTGC AGATCAAATT TCACGTCGTC TTCTGTATAC TGTGGAGGTA 1700

CACTCTTATA GAAAGTTCAA AAAGTCTACG CTCTCCTTTC TTTCTAACTC 1750

CAGTGAAGTA ATGGGGTCCT GCTCAAGTTG AAAGAGTCCT ATTTGCACTG 1800

TAGCCTCGCC GTCTGTGAAT TGGACCATCC TATTTAACTG GCTTCAGGCC 1850

TCCCCACCTT CTTCAGCCAC CTCTCTTTTT CAGTTGGCTG ACTTCCACAC 1900

CTAGCATCTC ATGAGTGCCA AGCAAAAGGA GAGAAGAGAG AAATAGCCTG 1950

CGCGGTTTTT TAGTTTGGGG GTTTTGCTGT TTCCTTTTAT GAGACCCATT 2000

CCTATTTCTT ATAGTCAATG TTTCTTTTAT CACGATATTA TTAGTAAGAA 2050

AACATCACTG AAATGCTAGC TGCAAGTGAC ATCTCTTTGA TGTCATATGG 2100

AAGAGTTAAA ACAGGTGGAG AAATTCCTTG ATTCACAATG AAATGCTCTC 2150

CTTTCCCCTG CCCCCAGAAC TTTTATCCAC TTACCTAGAT TCTACATATT 2200

CTTTAAATTT CATCTCAGGC CTCCCTCAAC CCCACGGGGC CGCCAGCACA 2250

CTGGAATTC 2259

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

    (A) LENGTH: 372 amino acids

    (B) TYPE: Amino Acid

    (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:


```
Met Ile Phe Pro Trp Lys Cys Gln Ser Thr Gln Arg Asp Leu Trp
1               5                   10                  15


Asn Ile Phe Lys Leu Trp Gly Trp Thr Met Leu Cys Cys Asp Phe
                20                  25                  30


Leu Ala His His Gly Thr Tyr Cys Trp Thr Tyr His Tyr Ser Glu
                35                  40                  45


Lys Pro Met Asn Trp Gln Arg Ala Arg Arg Phe Cys Arg Asp Asn
                50                  55                  60


Tyr Thr Asp Leu Val Ala Ile Gln Asn Lys Ala Glu Ile Glu Tyr
                65                  70                  75


Leu Glu Lys Thr Leu Pro Phe Ser Arg Ser Tyr Tyr Trp Ile Gly
                80                  85                  90


Ile Arg Lys Ile Gly Gly Ile Trp Thr Trp Val Gly Thr Asn Lys
                95                  100                 105


Ser Leu Thr Glu Glu Ala Glu Asn Trp Gly Asp Gly Glu Pro Asn
                110                 115                 120


Asn Lys Lys Asn Lys Glu Asp Cys Val Glu Ile Tyr Ile Lys Arg
```

125   130   135

Asn Lys Asp Ala Gly Lys Trp Asn Asp Asp Ala Cys His Lys Leu
                140   145   150

Lys Ala Ala Leu Cys Tyr Thr Ala Ser Cys Gln Pro Trp Ser Cys
                155   160   165

Ser Gly His Gly Glu Cys Val Glu Ile Ile Asn Asn His Thr Cys
                170   175   180

Asn Cys Asp Val Gly Tyr Tyr Gly Pro Gln Cys Gln Leu Val Ile
                185   190   195

Gln Cys Glu Pro Leu Glu Ala Pro Glu Leu Gly Thr Met Asp Cys
                200   205   210

Thr His Pro Phe Gly Asn Phe Ser Phe Ser Ser Gln Cys Ala Phe
                215   220   225

Ser Cys Ser Glu Gly Thr Asn Leu Thr Gly Ile Glu Glu Thr Thr
                230   235   240

Cys Gly Pro Phe Gly Asn Trp Ser Ser Pro Glu Pro Thr Cys Gln
                245   250   255

Val Ile Gln Cys Glu Pro Leu Ser Ala Pro Asp Leu Gly Ile Met
                260   265   270

Asn Cys Ser His Pro Leu Ala Ser Phe Ser Phe Thr Ser Ala Cys
                275   280   285

66

```
Thr Phe Ile Cys Ser Glu Gly Thr Glu Leu Ile Gly Lys Lys Lys
                290                 295                 300

Thr Ile Cys Glu Ser Ser Gly Ile Trp Ser Asn Pro Ser Pro Ile
                305                 310                 315

Cys Gln Lys Leu Asp Lys Ser Phe Ser Met Ile Lys Glu Gly Asp
                320                 325                 330

Tyr Asn Pro Leu Phe Ile Pro Val Ala Val Met Val Thr Ala Phe
                335                 340                 345

Ser Gly Leu Ala Phe Ile Ile Trp Leu Ala Arg Arg Leu Lys Lys
                350                 355                 360

Gly Lys Lys Ser Lys Arg Ser Met Asn Asp Pro Tyr
                365                 370     372
```

(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2214 base pairs
        (B) TYPE: Nucleic Acid
        (C) STRANDEDNESS: Single
        (D) TOPOLOGY: Linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:


```
GAATTCTCGA GCTCGTCGAC CACGCCCTCC TTGTGCAAGA ACTCTGAGCC 50

CCAGGTGCAG GAGGCTGAGG CCTGCAGAGA GACTTGCAGA GAGACCCAGC 100
```

AAGCCATGGT GTTTCCATGG AGATGTGAGG GTACTTACTG GGGCTCGAGG 150

AACATCCTGA AGCTGTGGGT CTGGACACTG CTCTGTTGTG ACTTCCTGAT 200

ACACCATGGA ACTCACTGTT GGACTTACCA TTATTCTGAA AAGCCCATGA 250

ACTGGGAAAA TGCTAGAAAG TTCTGCAAGC AAAATTACAC AGATTTAGTC 300

GCCATACAAA ACAAGAGAGA AATTGAGTAT TTAGAGAATA CATTGCCCAA 350

AAGCCCTTAT TACTACTGGA TAGGAATCAG GAAAATTGGG AAAATGTGGA 400

CATGGGTGGG AACCAACAAA ACTCTCACTA AGAAGCAGA GAACTGGGGT 450

GCTGGGGAGC CCAACAACAA GAAGTCCAAG GAGGACTGTG TGGAGATCTA 500

TATCAAGAGG GAACGAGACT CTGGGAAATG GAACGATGAC GCCTGTCACA 550

AACGAAAGGC AGCTCTCTGC TACACAGCCT CTTGCCAGCC AGGGTCTTGC 600

AATGGCCGTG GAGAATGTGT GGAAACTATC AACAATCACA CGTGCATCTG 650

TGATGCAGGG TATTACGGGC CCCAGTGTCA GTATGTGGTC CAGTGTGAGC 700

CTTTGGAGGC CCCTGAGTTG GGTACCATGG ACTGCATCCA CCCCTTGGGA 750

AACTTCAGCT TCCAGTCCAA GTGTGCTTTC AACTGTTCTG AGGGAAGAGA 800

GCTACTTGGG ACTGCAGAAA CACAGTGTGG AGCATCTGGA AACTGGTCAT 850

CTCCAGAGCC AATCTGCCAA GTGGTCCAGT GTGAGCCTTT GGAGGCCCCT 900

68

GAGTTGGGTA CCATGGACTG CATCCACCCC TTGGGAAACT TCAGCTTCCA 950

GTCCAAGTGT GCTTTCAACT GTTCTGAGGG AAGAGAGCTA CTTGGGACTG 1000

CAGAAACACA GTGTGGAGCA TCTGGAAACT GGTCATCTCC AGAGCCAATC 1050

TGCCAAGAGA CAAACAGAAG TTTCTCAAAG ATCAAGAAG GTGACTACAA 1100

CCCCCTCTTC ATTCCTGTAG CCGTCATGGT CACCGCATTC TCGGGGCTGG 1150

CATTTCTCAT TTGGCTGGCA AGGCGGTTAA AAAAAGGCAA GAAATCTCAA 1200

GAAAGGATGG ATGATCCATA CTGATTCATC CTTTGTGAAA GGAAAGCCAT 1250

GAAGTGCTAA AGACAAAACA TTGGAAAATA ACGTCAAGTC CTCCCGTGAA 1300

GATTTTACAC GCAGGCATCT CCCACATTAG AGATGCAGTG TTTGCTCAAC 1350

GAATCTGGAA GGATTTCTTC ATGACCAACA GCTCCTCCTA ATTTCCCTC 1400

GCTCATTCAT CCCATTAACC CTATCCCATA ATGTGTGTCT ATACAGAGTA 1450

GTATTTTATC ATCTTTTCTG TGGAGGAACA AGCAAAAGTG TTACTGTAGA 1500

ATATAAAGAC AGCTGCTTTT ACTCTTTCCT AACTCTTGTT TCCTAGTTCA 1550

ATTCAGCACA GAAGCTAATG CCAAACACAG TGAAAATATG ATCCATGAGT 1600

AATTGGAAAC TCAGACTCCT TGCGCATAGT ACGTACCCTA TGTAACATCG 1650

ACAAAAATCT TTCATTTCCA CCTCCAAAGA ACAGTGCTCT ATTCAAGTTG 1700

GGAAAGTCCT ACTTCCTCTG TAGACCCACT ATCTGTGAGT GACAGCCACT 1750

GTAGCTGTTC ACATTAACCT TCCCCATCTC CTTTTCCTAG GAGAATAATT 1800

CCACACACTG CACCCCATGA TGGCCACCAA ACATCAAAGA AGGGAAAATC 1850

TCCTGCATTG AGTTTTAGTT TTGAGTTTTC CCTTCTCTTT ATTAGATCTC 1900

TGATGGTTCC TTGAAGTCAG TGTTCTGATG ATTATTAATA GTTAATGATA 1950

ACACAACCCA CTCTCTTGGA GCTGATGTTA TGAAGACAAC AGGTAGAAAA 2000

ATTCCTGGGC TCAGGCTGGA GTGACACCCT TTTCTTTCCC TAACATCTTC 2050

TACTCAGATA CCTAAATTTA AGATTCAGGA CAGCTGTCCC CAACTCTTAC 2100

CATGTCTTTT ATAACTTGCT CCTTAACTTG CCCAACCTGT AGGCTATCTC 2150

ATTTTCTCGC TTCACTCTGC AAGGTTTATA ACATGATGAA TTTAAATACA 2200

AAAAAAAAAA AAAA 2214

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 372 amino acids
        (B) TYPE: Amino Acid
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Val Phe Pro Trp Arg Cys Glu Gly Thr Tyr Trp Gly Ser Arg

70

```
          1                    5                   10                   15

     Asn Ile Leu Lys Leu Trp Val Trp Thr Leu Leu Cys Cys Asp Phe
                    20                   25                   30

     Leu Ile His His Gly Thr His Cys Trp Thr Tyr His Tyr Ser Glu
                    35                   40                   45

     Lys Pro Met Asn Trp Glu Asn Ala Arg Lys Phe Cys Lys Gln Asn
                    50                   55                   60

     Tyr Thr Asp Leu Val Ala Ile Gln Asn Lys Arg Glu Ile Glu Tyr
                    65                   70                   75

     Leu Glu Asn Thr Leu Pro Lys Ser Pro Tyr Tyr Tyr Trp Ile Gly
                    80                   85                   90

     Ile Arg Lys Ile Gly Lys Met Trp Thr Trp Val Gly Thr Asn Lys
                    95                  100                  105

     Thr Leu Thr Lys Glu Ala Glu Asn Trp Gly Ala Gly Glu Pro Asn
                   110                  115                  120

     Asn Lys Lys Ser Lys Glu Asp Cys Val Glu Ile Tyr Ile Lys Arg
                   125                  130                  135

     Glu Arg Asp Ser Gly Lys Trp Asn Asp Asp Ala Cys His Lys Arg
                   140                  145                  150

     Lys Ala Ala Leu Cys Tyr Thr Ala Ser Cys Gln Pro Gly Ser Cys
                   155                  160                  165
```

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Asn Gly Arg Gly Glu Cys Val Glu Thr Ile Asn Asn His Thr Cys
              170   175   180

Ile Cys Asp Ala Gly Tyr Tyr Gly Pro Gln Cys Gln Tyr Val Val
              185   190   195

Gln Cys Glu Pro Leu Glu Ala Pro Glu Leu Gly Thr Met Asp Cys
              200   205   210

Ile His Pro Leu Gly Asn Phe Ser Phe Gln Ser Lys Cys Ala Phe
              215   220   225

Asn Cys Ser Glu Gly Arg Glu Leu Leu Gly Thr Ala Glu Thr Gln
              230   235   240

Cys Gly Ala Ser Gly Asn Trp Ser Ser Pro Glu Pro Ile Cys Gln
              245   250   255

Val Val Gln Cys Glu Pro Leu Glu Ala Pro Glu Leu Gly Thr Met
              260   265   270

Asp Cys Ile His Pro Leu Gly Asn Phe Ser Phe Gln Ser Lys Cys
              275   280   285

Ala Phe Asn Cys Ser Glu Gly Arg Glu Leu Leu Gly Thr Ala Glu
              290   295   300

Thr Gln Cys Gly Ala Ser Gly Asn Trp Ser Ser Pro Glu Pro Ile
              305   310   315

Cys Gln Glu Thr Asn Arg Ser Phe Ser Lys Ile Lys Glu Gly Asp
              320   325   330

72

```
Tyr Asn Pro Leu Phe Ile Pro Val. Ala Val Met Val Thr Ala Phe
            335             340             345

Ser Gly Leu Ala Phe Leu Ile Trp Leu Ala Arg Arg Leu Lys Lys
            350             355             360

Gly Lys Lys Ser Gln Glu Arg Met Asp Asp Pro Tyr
            365             370     372
```

(2) INFORMATION FOR SEQ ID NO:5:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 38 amino acids
        (B) TYPE: Amino Acid
        (D) TOPOLOGY: Linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
Xaa Thr Tyr His Tyr Ser Glu Lys Pro Met Asn Trp Glu Asn Ala
  1             5               10                      15

Arg Lys Phe Xaa Lys Gln Asn Tyr Thr Asp Leu Val Ala Ile Gln
            20              25                      30

Asn Lys Xaa Xaa Ile Glu Tyr Leu
            35              38
```

(2) INFORMATION FOR SEQ ID NO:6:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 26 base pairs
        (B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAGAAGCCCA TGAATTGGGA GAATGC 26